us-09-497-967-1.rge

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GenCore version 5.1.3
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OM nucleic - nu	nucleic search, using sw model
Run on:	3, 15:
Title: Perfect score: Sequence:	US-09-497-967-1 1326 1 atgaaatataatattttattttatttctttctatttatt
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:*  1

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		os Ouerv			SUMMARIES	
:	Score	Match	Length	DB	QI	ton
7	1326	0.0	2486	m	AF140273	74007
2 1	170.4	88.3	1249	m	ICYIMANT	1
	647.2	æ.	1520	m	AF405431	AF405431 Ichthyoph
41	D.	6	3026	m	AF324424	AF324424 Ichthi
ט נ	4.0	7.	1312/4	N 0	AC096869	AC096869 Rattus no
	70	7 -	176037	חר	AL3632/2	AL365272 Human I
	6	. C	179553	4 (	AC0341/4	Rattu
σ	89.8	. «	170985	٠,	AC096032	AC024233 HOMO SA
c 10	88.8	۲.	186935	N	AC022322	משטק
11	88.4	۲.	189461	7	AC119627	AC119627 Pattus
12	88.4	۲.	191841	7	AC121374	AC121374 Battus
13	87.6	۰.	204259	~	AC110817	AC110817 Mis miscus
1.4	87.6	9	264522	~	AC090437	0 0 2 2 2 2
15	86.2	r.	84472	~	AC096684	7 8 T
c 16	83.8	3	1611	10	MMU70651	U70651 Mus muscul
	82.6	3	172307	7	AC044842	AC044842 Homo s
	82.6	7	201470	7	AC113649	AC113649 Rattus no
	82.4	ď	149228	7	AC113774	AC113774 Rattus
c 20	82.4	ď	261604	7	AC119819	AC119819 Mus mu
	82.2	N	165318	~	AC126747	AC126747 Rattus
	81.8	CJ.	175699	~	AC129136 .	AC129136 Rattus
c 23	81.6	~	131346	~	AC119558	AC119558 Rattus
		0	88203	S.	AC097628	AC097628 Takifugu
57.0	4.6	0	176774	(7)	AC1.09366	AC109366 Rattus
	2,5	0	209973	~	AC073755	AC073755 Mus mu
200	7.87	ν c	71553	~	AC096997	AC096997 Takifugu
	70.7	ν c	1,5/48	N (	AC120669	AC120669 Rattus
	7.07	ν α	1613	٠, <sup>۲</sup>	AC125859	$\sim$
	77.4	α	196650	3 6	AC111317	U/U652 Mus muscul
	77.2	œ	85786	٥σ	ACILIZI/ AI.162582	ACILIZI/ RATTUS DO
33	77	α	186380	·σ	AC100822	AL100822 Human
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35	76.6	α	180668	0	AC020857	ACOSOBS7 Mus muse.
36	w	1	183413	10	AC131200	and and
c 37		~	168757	ı c	AC127508	משטן
	75.6	7	87201	0	AC007623	ACOOTES HOME BURL
39	ഗ	~	172853	0	AC084361	
	75.4	~	185994	~	AC002042	
c 41	ഗ	^	186558	2	AC079031	
42	75	7	216977	7	AC105611	1
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c 44	74.8	9	325808	~	AC121787	
45	4	9	108476	7	AC094507	
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RESULT 1						
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ACCESSION		48) gen 0273	(IAG48) gene, compared AF140273	complete	cds.	ı antıgen precursor
KEYWORDS	AF 14	02/3.I	G1:48	:4868370	o.	
SOURCE		Ichthyophthirius		nult	multifiliis.	
ORGANISM		hyophth		nult	filits	

Eukaryota: Alveolata; Ciliophora; Oligohymenophorea; Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 2486)
Clark, T.G., Lin, T.L., Jackwood, D.A., Sherrill, J., Lin, Y. and Dickerson, H.W. REFERENCE AUTHORS

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                                                                                                                              3 (bases 1 to 2486)
Clark, T.G., Lin, T.-L., Jackwood, D.A. and Dickerson, H.W.
Direct Submission
Submitted (29-MAR-1999) Microbiology & Immunology, Cornell
Submitted (29-MAR-1999) Microbiology & Immunology, Cornell
University, College of Veterinary Medicine, Ithaca, NY 14853, USA
                                                                        Gaertig, J., Gao, Y., Tishgarten, T., Clark, T.G. and Dickerson, H.W. Surface display of a parasite antigen in the ciliate Tetrahymena
protein predicts tandemly
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/organism="Ichthyophthirius multifillis"
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100.0%; Pred. No. 6.1e-241;
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for an abundant parasite coat
e metal binding domains
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IChthyophthirius multifiliis immobilization antigen precursor,
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Submitted (18-SEP-1998) Microbiology and Immunology, Cornell
Gulversity, Ithaca, NY 14853, USA
Sequence update by submitter
On Sep 18, 1998 this sequence version replaced gi:159289.
Location/Qualifiers
1. 1249
/organism="Ichthyophthirius multifilis"
                                                                                                                                                                                                                                                      of immobilization
                                                                                                                                                                                                                                                                                                                                Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Developmental expression of surface antigen genes in the ciliate Ichthyophthirius multifillis
Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-JUN-1992) Microbiology and Immunology,
University, Ithaca, NY 14853, USA
( pases 1 to 1249)
                                                                                                                                                                         Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius. Li (bases 1 to 1249)
Lin, T.L. and Dickerson, H.W. Purification and partial characterization of immobil antigens from Ichthyophthirius multifiliis
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177. Aoa
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  Length 1249;
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  DB 3;
 Score 1170.4; DB 3
Pred. No. 1.8e-211;
0; Mismatches 1;
 88.3%;
99.9%;
Query Match 88.3
Best Local Similarity 99.9
Matches 1171; Conservative
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                                                                                                                                                                                                                                                                                                                               AF405431 1620 bp mRNA linear INV 27-FEB-2002 Ichthyophthirius multifillis 52kDa immobilization antigen variant B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variation in primary sequence and tandem repeat copy number among i-antigens of Ichthyophthirius multifiliis
Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 1520)
Lin, Y., Lih, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R. and Clark, T.G.
                       1021 TTGATGAAGAACATCAACTAATTTTGTAGCTTCCGCAACTGAATGTACTAAATGTTCTG 1080
                                                                                                        GTTCCATGTCCTGATGGTACTTAGACTCAAGCTGGATTGACTGATGTAGGTGCTGCTGAT 120
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                                                                                      1136 CTGGCTTTTTTGCATCAAAACAACTGGTTTTACAGCAGGTACTGATACATGTACTGAAT
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Pred. No. 1.4e-112;
0; Mismatches 343;
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Lin,Y., Wang,J.C. and Clark,T.C.
Direct Submission
Submitted (03-AUG-2001) Microbiology
University, Ithaca, NY 14853, USA
Location/Qualifiers
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GAAGCTAATGGTAATTAACCTTTCGCAGCAATAATGCTGCTAGAGGTATATGTGTACCA
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                                                 CTTGGTACTTGTGTAATTGCAGACCTAATTTTTACTATAATGGTGGTGCTGCTTAAGGA
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                                                                                                                                                                                                                                                           Ichthyophthirius multifiliis immobilization antigen isoform AF324424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin.Y., Lin.T.-L. and Clark,T.G.
Direct Submission
Submitted (27-NOV-2000) Microbiology and Immunology, NYSCVM Cornell
University, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATDYAAIITECVNCRINFYNENAPNFNAGASTCTACPVNRYGGALTAGNAATIVAO
VNACPTGALDDGVTTDYVBSFTECVKCRLNFYYNGNNGNTPFNPGKSQCTPCPAIK
PANVAGATLGNDATITAGCNVACPDGISAAGVNWYAQNTECTNCAPNFYNNNTANPNF
NPGNSTCLPCPANKDYGAEATAGGAATLAGCNINCPGTAIASGATNYYLLGTECLN
CAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAGTYLTDGT
TSTYKQAASECVKCAANFYTTKQTDMVAGIDTCTSCNKKLTSGAEANLPESAKKNIQC
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VNCQKNFYYNNAAAFVPCASTGTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTAIA
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 3026). Lin.Y. Lin.T. Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R. and Clark, T.G.
and Clark, T.G.
Variation in primary sequence and tandem repeat copy number among
1-antigens of Ichthyophthirius multifillis
Mol. Blochem. Parasitol. 120 (1), 93-106 (2002)
GTTGATGATGGTACATCAACTATTTTGTAGCTTTAGCAAGTGAATGTAATGTTAG 1228
                                        1254
                         GCTGGCTTTTTTGCATCAAAACAACTGGTTTTACAGCAGGTACTGATACATGTACTGAA
                                                                           TGTACTAAAAAATTAACTTCTGGTGCCACAGGTAAAGTATATGCTGAAGGTACTCAAAAA
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.
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1330. ,2736
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/protein_id="AAK01661.1"
/db_xref-"GI:12698727"
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/db_xref="taxon:5932"
1285. .2817
/gene="IAG52A"
1285. .2817
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/gene="IAG52A"
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1673 GIGTTAATTGTAGAATTAATTTTTATAATGAAAATGCTCCAAATTTTAATGCAGGTGCTA 1732
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                                                                                                                                           GTGCTGCTTAAGGAGAAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTG 466
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                                                                                                        Gaps
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                                                                                                                                                                                                                         GTATATGTGTACCATGCCAAATAAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAG
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                                                                                                      394; Indels 111;
                                                                 Length 3026;
                                                               DB 3;
                                                                                  , 6e-38;
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Best Local Similarity 56.7%;
Matches 660; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                 1181 ATACATGTACTGAATGTACTAAAAATTAACTTCTGGTGCCACAGCTAAAGTATATGCTG 1240
2537 GIGITAAAIGIGCIGCCAACTITIAIACTACAAAAIAAACIGAIIGGGIAGCAGGIAIIG 2596
                                                                                                                                                                              Grovemont Circle, Gaithersburg, MD 20877, USA
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                                                                                                2597 ATACATGTACTAGTTGTAATAAAAATTAACTTCTGGCGCTGAAGCTAATTTACCTGAAT
                                                                                                                                                       1241 AAGCTACTCAAAAAGTATAATGCGCCTCCACTACTTTCGCTAAATTTTTATCGATTTCCT
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Submitted (29-SEP-2001) NIH Intramural
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Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
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Center clone name: 289D09
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Rattus norvegicus.
                                                                                                                                                                                                                                                                                      2708 TATTATTGATTTCTTATTATTTATT 2732
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49334 GITGGTGCTGCTGCTGCTGCTGCTGCTGCTGATGCTGCTGGTGCTGCTGCTGGT 49275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACCTAACTTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GGAGAAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAGGTATATGTGTA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 CCATGCCAAATAAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GCTGTTCCATGTCCTGATGGTACTTAGACTCAAGCTGGATTGACTGATGTAGGTGCTGCT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GATCTTGGTACTTGTGTTAATTGCAGACCTAATTTTTACTATAATGGTGGTGCTGCTTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 GTTGCTGCCGTTACTAGTTAATGTGTACCTTGCCAACTAAACAAAAACGATTCTCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 ACTGCAGGIGCCTAAGCTAATTTAGCCACATAATGTAGCAATTAATGTCCTACTGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACTTGATGATGGAGTGACACTTGTTTTTAATACATCAGCCACATTATGTGTTAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 ACATAATGCAGTACTTAATGTCCTACTGGCACTGCACTTGATGATGGAGTGACAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 TTTGATAGATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTACTATAATGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 TCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTGCCGCTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131274;
1 4803: contig of 4803 bp in length
4904 3332: contig of 28429 bp in length
1333 33432: gap of unknown length
1433 74914: contig of 41482 bp in length
155 75014: gap of unknown length
165 131274: contig of 56260 bp in length
165 Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 2; 1
Pred. No. 2.1e-08;
0; Mismatches 380;
                                                                                                                                                                       1. .131274
/organism="Rattus norvegicus"
/strain="Brown Norway"
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/note="assembly_fragment"
27361 c 27739 g 38239 t
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                                                                                                                                                                                                                                                                                                   /note="assembly_fragment" 4904. .33332
                                                                                                                                                                                                                /db_xref="taxon:10116"
/clone="RP31-289D9"
/clone_lib="RP31"
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2475. .4279 /note="L1M4 14306. .4589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submitted (23-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk munquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone sasembly data is compared from overlapping clones. Where differences are found these are annotated as variations squence assembly data is compared from overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, annotated repeat sequence elements. Where the sequence is numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information thttp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping http://www.anger.ac.uk/HGP/Chr6

Group. Further information can be found at Chromosome 6 mapping http://www.anger.ac.uk/HGP/Chr6

RRII-38CI7 is from the library RPCI-II.2 constructed by the group http://www.chori.org/bacpac/home.htm

WETOR: PBACES.
                                                                                                                                                                                                                                         AL365272 132449 bp DNA linear PRI 23-DEC-2000
Human DNA sequence from clone RPI1-328C17 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-328C17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-328C17 is at 132449 in this sequence. The true left end of clone RP11-233X4 is at 64893 in this sequence. The true right end of clone RP3-416J7 is at 100 in this sequence. The true right end of clone RP3-416J7 is at 160 in this sequence. The true right end of clone RP1-125A24 is at 61243 in
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132449)
49154 GGTGCTGGTGCTGCTGGTGGTACTTTGGTGCTGGTGCTGGTGCTGGTGCTGGTGCTGCT 49095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3937 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2200. .2474
/note="AluSx repeat: matches 38. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .80 of consensus"
                                                                                 49094 GGTGCTGCTGGTGCTGCTGCTGTTGGTGCTGGTGCT 49053
                                                   718 TTTGCTGCTGGTGCTGCCGCTGCAGGTGTTGCTGCCGTTACT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1669 .2199
/note="LIM4 repeat: matches 3396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1563. .1641
/note="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.2"
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AL365272.20 GI:11991402
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AL365272/c
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DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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7435. 3034

7001e="LiM4" repeat: matches 272. .420 of consensus" complement(5020. 5329)

7001e="match: GSS: Em:AQ494601"

7142. .5435

7001e="MLTID repeat: matches 170. .428 of consensus" 5436. .574

7001e="MLTID repeat: matches 1. .310 of consensus" 5745. .5869

7001e="MLTID repeat: matches 428. .568 of consensus" 6450. .6686

7001e="MLTID repeat: matches 7. .261 of consensus" 701e="MIM repeat: matches 7. .261 of consensus" 701e="LiM4" repeat: matches 3582. .4688 of consensus" 7984. .8050

7001e="LiM4" repeat: matches 3808. .5884 of consensus" 7984. .8050

7001e="LiM5" repeat: matches 3808. .5884 of consensus" 7984. .8050

8178. .8169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8178. .8224 --reach matches 4479. .3593 of consensus" /note="LIMMA repeat: matches 6124. .6169 of consensus" 8225. .8528 /note="Alusx repeat: matches 1. .301 of consensus" 6526. .8918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8526. .8915
/note="LiMB4 repeat: matches 5725. .6124 of consensus"
complement(8862. .9353)
repeat: matches 1686. .3396 of consensus"
                                                .1544 of consensus"
                                                                                                                                             .924 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2668. .2749 of consensus" 15876. .15935 /note="2 copies 30 mer 100% conserved" 16202. .16294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Aluy repeat: matches 1. .309 of consensus"
12109. 12515
17019. 12517
17019. 12547
17019. 12547
17019. 12017
17019. 12017
17019. 12017
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13331. .13664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MLT1B repeat: matches 4, ,361 of consensus"
3704, ,13907
note="LTR33 repeat: matches 297, 511 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .237 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 297. .511 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9029. .9150
/note="2 copies 61 mer 95% conserved"
complement(9052. .9484)
                 4306. .4589
/note="L1M4 repeat: matches 1254.
complement(4704. .5324)
                                                                                                                 4799. 4938
Anote "Linko repeat: matches 785.
complement(4809. 5326)
/note = "match: GSS: Em:AQ774852"
                                                                    complement(4704. .5324)
/note="match: GSS: Em:AQ628183"
                                                                                                                                                                                                            complement(4860. .5272)
/note="match: GSS: Em:AQ787689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(9052. ,9484)
note="match: GSS: Em:AQ175845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9388, 9675
/note="match: GSS: Em:AQ135206"
9487, 9840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8862, .9353)
/note="match: GSS: Em:AQ355497"
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13005. .13103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9487. .9840
/note="match: GSS: Em:AQ717684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9491. .9932
/note="match: GSS: Em:AQ147759"
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'note="L2 repe
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/woute="-cpu islaminated contemplated contem
                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 42. .152 of consensus" 22328. .22772 /note="L2 repeat: matches 2242. .2710 of consensus" 20168. .22848 /note="L2 repeat: matches 2661. .2750 of consensus" 23314. .24204 /note="CpG island"
                                                                                                                                                               /note="match: GSS: Em:AQ151578"
19374. 19496
/note="L2 repeat: matches 2579. .2709 of consensus"
20271. .20430
/note="marR20 repeat: matches 55. .218 of consensus"
21095. .21389
                                                                                                                                                                                                                                                                                                                                                    ,295 of consensus"
                                                                                                                of consensus'
of consensus'
                                                                                                                . 296
                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1.
21830. .21946
                                                 /note="match: GSS: Em:AQ104665"
17419. 17715
/note="AluSx repeat: matches 1.
17995. 18362
repeat: matches 2.
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2; Gaps 0; Mismatches 650; Indels 15; Score 94; DB 9; Length 132449; Pred. No. 2e-08; Best Local Similarity 43.8%; Matches 519; Conservative Query Match

Db 103814 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTCCTGCCA 103755 CTGATGGTACTTAGACTCAAGCTGGATTGACTGATGTAGGTGCTGCTGATCTTGGTACTT 130

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1205 AATTAACTTCTGGTGCCACACTAAAGTATATGCTGAAGCTACT 1248 Οy GIGITAATIGCAGACCTAATITITACTATAATGGIGGTGCTGCTTAAGGAGAAGCTAATG 190

102923 CIGCAACIGCIGATGCIGCIACICCIGCCACAGCIACIGCAACIGCIGCIGCIGCIA 102864 102983 CTACTCCTCCCACACGCTACTGCTGCTGTGCTGCTGCTCCTCCTGCCACACGCTA 102924 102863 CTCCTGCCACAGCTACTGCAACTGCTGCTGCTGCTGCCACAGCTACTGCAACTG 102804 DD 103163 CTCCTCCTGCCACAGCTACTGCAACTACTGATGCTGCTACTCCTGCCACAGCTACTGCAA 103104 103103 CTGCTGATGCTGCTACTCCTGCCACCACCAACTGCTGCTGCTGCTGCTCTC 103044 Db 103043 CTGCCACAGCTGCAACAGCTGCTGCTACTCCTGCCACAGCTACTGCAACTGCTG 102984 103403 TIGCAACTGCTGCTGCCACAGCTACTGCAACTGCTACTACTGCTGCTGCAA 103344 Db 103343 cadcinacidechacidecideridecracitectecidechaciaechacidenacidard 103284 Db 103223 CTGCAACTGCTGCTACTCCTCCTGCCACAGCTACTGCAACTGCTGCTGCTGCTA 103164 Db 103634 CTGCAACTGCCGATGCTGCTACTCCTCGCCACAGCTGCTGCAACTGCCGATGCTGCTA 103575 Db 103463 CTACTCCTCCTGCACAGCTACTGCAGATGCTGCTACTCCTCCTGCCACAGCTA 103404 DD 103754 CAGCTACTGCCATGCTGCTACTCCTGCCACGCTACTGCCGATGCTG 103695 Db 103694 CTACTCCTCCTGCCACAGCTGCTGCCATGCTGCTCCTCCTGCCACAGCTG 103635 971 AATGITTAAAGIGTCCAGTAAGTAAAACTACTCCAGCACATGCTCCAGGTAATACTGCTA 1030 1031 CITAAGCCACATAAIGITIGACCACATGICCIGCIACGTACAGTACTIGAIGAIGAACAI 1090 CAACTAATTTTGTAGCTTCCGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTTGCAT 1150 CAAA-----AACAACTGGTTTTACAGCAGGTACTGATACATGTACTGAATGTACTAAAA 1204 791 ACGATICICCIGCCACIGCAGGIGCCIAAGCIAATTTAGCCACAIAATGCAGTACTIAAT 850 851 GTCCAACTGGCACTGCAATTCAAGACGGAGTGACACTTGTTTTTAGTAATTCATCCACAT 910 GTAATTAACCTITCGCAGCAAATAATGCTGCTAGAGGTATATGTGTACCATGCCAAATAA 250 611 GAGTGACACTTGTTTTTAATACATCAGCCACATTATGTGTTAAATGCAGACCTAACTTTT 103283 CIGCIACTGCCACAGCTACTGCAACTGCTGATGCTGCTACTCCTCCTGCCACAGCTA ACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTG CTGCCGCTGCAGGTGTTGCTGCCGTTACTAGTTAATGTGTACCTTGCCAAATAAACAAAA 911 AATGTTCTTAATGCATTGCTAATTACTTTTTTAATGGTAATTTCGAAGCAGGTAAAGTT AAGCTAATTTAGCCACATAATGTAGCAATTAATGTCCTACTGGCACTGTACTTGATGATG CITAATGTCCTACTGGCACTGCACTTGATGGAGTGACAGATGTTTTTGATAGATCAG 431 AAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTGCCGCTGCAGGTGTTGCTGCCGTTA CTAGTTAATGTGTACCTTGCCAACTAAACAAAAACGATTCTCCTGCCACTGCAGGTGCCT 251 ACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCCACATAATGCAGTA CCGCATAATGTGTTTAAATGCAAACCTAAACTTTTACTATAATGGTGGTTCTCCTTAAGGTG 731 1091 1151 551 671 491 311 371 191 g δλ 9 Dp QΫ́ ò Ω ŏ ōλ ŏ ολ δy Qy Qγ ΩŊ Ω QΥ

## Db 102683 CIGCTACTCCTCCTGCCACAGCTACTGCAACTGCTGCTGCTGCT 102640

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Alstrooks, S.L. Anaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blatchoroks, S.L., Anaratunge, H.C., Are, J.R., Ayele, M., Banth, D., Barbaria, J. Benton, J., Blanchurg, K., Bonnin, D., Bouk, J., Benton, J., Blanchurg, K., Bonnin, D., Bouk, J., Berver, B., Brown, M., Bryant, N. P., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Char, C., Burd, M. C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, C., Chen, C., Davy-Carroll, L., Dederich, D.A., David, R., Dring, R., Marting, R., Dring, R., Marting, R., Marting, R., Marting, R., Marting, R., Dring, R., Marting, R., Ma
                        ACCUSALIA 176822 bp DNA linear HTG 12-JUL-2002 Rattus norvegicus clone CH230-9811, *** SEQUENCING IN PROGRESS ***, Account
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Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18846108.
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                                                                                                                                                                                                                                                                                                         Eukaryota; Métazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE1.
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Rattus norvegicus
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 77 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
            Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contect: hgsc-help@bcm.tmc.edu
Contect: hgsc-help@bcm.tmc.edu
Center project Information
Center clone name: GR20-8811
Center clone name: GH230-8811
Center clone name: CH230-8811
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s. contig of 2802 bp
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gap of unknown l
contig of 1547 b
gap of unknown l
contig of 1064 b
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Homo sapiens chromosome 6 clone RP11-758C19, WORKING DRAFT SEQUENCE, 12 unordered pieces.
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Waterston, R.H.
Direct Submission
Submitted (28-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:8568958.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179553)
Waterston, R. H.
                                                                                                                                                                         175070 GCTGGTACTGCTGGTGCTGGTGCTGCTGCTGCTGGTGCTGCTGGTGCTGGT 175011
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                                          CCATGCCAAATAAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTATTAGCC
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                                                                                                   298 ACATAATGCAGTACTTAATGTCCTACTGGCACTGCACTTGATGGAGTGACAGATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Genome Center
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ATG24253.4 GI:9959959
HTG; HTGS_PHASEL; HTGS_DRAFT.
HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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TITLE
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Pirzep; version 0.990319
Consensus quality: 17523 bases at least Q40
Consensus quality: 17523 bases at least Q30
Consensus quality: 17711 bases at least Q20
Insert size: 198000; agarose-fp
Insert size: 178453; sum-of-contigs
Quality coverage: 4.48 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                    4: contig of 7554 bp in length
4: gap of unknown length
9: gap of unknown length
5: contig of 10026 bp in length
5: gap of unknown length
0: contig of 10026 bp in length
0: contig of 3305 bp in length
0: gap of unknown length
0: gap of unknown length
0: gap of unknown length
1: contig of 28455 bp in length
2: contig of 28455 bp in length
5: gap of unknown length
6: gap of unknown length
9: contig of 45736 bp in length
9: contig of 45736 bp in length
8: contig of 45736 bp in length
9: contig of 45736 bp in length
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9: contig of 2274 bp in length
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/note="assembly_name:Contig14"

62111. .90565

/note="assembly_name:Contig15"

90666. .117183

/note="assembly_name:Contig16"

117284. .163019
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7655. 16349
7600te="assembly_name:Contig11"
16450. 26475
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163120, 166938
/note="assembly_name:Contig8
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169413. .171639
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171740, .179553
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167039. .169312
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174935 TGCTGCTACTGCTGCTGGTGTTGCTACTGTTGCTACTATGGTAATTATTGCTGC 174994
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                                                                                                                                                                                                                                     AGCTGGATTGACTGATGTAGGTGCTGCTGATCTTGGTACTTGTTAATTGCAGACCTAA 149
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                                                                                                                                                                                                                                                                                                                                                                                             210 AAATAATGCTGCTAGAGGTATATGTGTACCATGCCAAATAAACAGAGTAGGCTCTGTTAC
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                                                                             Score 93; DB 2; Length 179553;
Pred. No. 3e-08;
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/note="assembly_name:Contig9"
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Muzny, D.M., Adams, C., Addio-Oduola, B. Ali-Osman, F.R., Allen, C., Alison, C., Addio-Oduola, B. Ali-Osman, F.R., Allen, C., Alisonoka, S. Mishage, K., Blankenburg, K., Bonnin, D., Burbai, J., Benton, J., Bargae, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, S., Biteva, M., Brown, E., Brown, M., Bryant, N.P., Burbay, C., Burch, P., Burkett, C., Burrell, K.L., Byda, N. Bryant, N.P., Chan, C., Coyle, M.D., Dathorne, S. R., David, R., Chen, G., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgaco, O., Denn, A.L., Ding, Y., Dinh, H.H., Garnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bacctto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bacctto, M., Gao, J., Garcia, A., Garza, N., Garza, N., Gill, R., Garis, J., Garo, J., Garcia, A., Garza, M., Garier, Y., Hale, S., Hamilton, K., Garis, R., Harland, M., Gacker, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Uoudah, S., Jondon, S., Huber, J., Johnson, R., Jolivet, S., Joudah, S., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martinez, E., Massey, E., Mawhiney, E., McLed, B., Watting, R., Massey, E., Mawhiney, E., McLed, M., Meil, G., Morez, M., Nolyen, N., Nickerson, E., Newten, S., Oguh, M., Okwuon, G., Miner, S., Miner, S., Mitch, M., Palas, M., Palas, N., Perez, L., Pickens, R., Palas, M., Palas, M., Palas, S., Soctt, G., Shen, H., Specker, P., Tamerisa, K., Tangey, J., Taylor, C., Taylor, T., Talfrod, B., Thomas, N., Tangey, J., Taylor, C., Palas, W., Walliams, G., Walliams, G., Walliams, G., Walliams, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 11-JUL-2002
                                                                                                             DD 175760 TATIGITGCIGATGCIGCIACTGTIGCIGITGCIGCIACTACTGTIGCIGITGCIACT 175819
                                                                                                                                                                                                                                      DD 175880 IGCTGCTGCTGCTGCTGTTGTTGCTACTGCTACTTCTGTTGCTGCTGCTGCTGC 175939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
DD 175703 GGCTGCTATTATTGTTGC---TGCTGCTGTTGCTGTTACTGCTGCTATTGTTGCTGT 175759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACUYBU32 170985 bp DNA linear HTG 11-JUL-2
Rattus norvegicus clone CH230-37D13, *** SEQUENCING IN PROGRESS
***, 76 unordered pieces.
                                                                           1050 GACCACATGTCCTGCTGGTACAGTACTTGATGGAACATCAACTAATTTTGTAGCTTC 1109
                                                                                                                                                                                   1110 CGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTTGCATCAAAACAACTGGTTTTAC 1169
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KEYWORDS
SOURCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 76 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                   Substituted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 170985) Worley, K.C. Direct Submission (11-UL-2002) Human Genome Sequencing Center, Department Submitted (11-UL-2002) Human Genome Sequencing Center, Department Submitted (11-UL-2002) Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:20976008.
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s; gap of unknown length
l: contig of 1255 bp in length
s; contig of 1257 bp in length
s; contig of 1257 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186935)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                          107565 GTTGCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGTTGCTGTTGCTGTTT 107624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 107865 GITGCIGCIGCIGCIGCTGTTGCIGCIGITGCIGCIGTTGCTGATGITGCIGATGTTGCT 107924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GGAGAAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAGGTATATGTGTA 237
                                                                                                                                  58 GCTGTTCCATGTCCTGATGGTACTTAGACTCAAGCTGGATTGACTGATGTAGGTGCTGCT 117
                                                                                                                                                                                                     118 GATCTTGGTACTTGTGTTAATTGCAGACCTAATTTTTACTATAATGGTGGTGCTGCTTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 TTTGATAGATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTACTATAATGGTGGT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 TCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTGCCGCTGCAGGT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 GTTGCTGCCGTTACTAGTTAATGTGTACCTTGCCAACTAAACAAAAACGATTCTCCTGCC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 ACTGCAGGTGCCTAAGCTAATTTAGCCACATAATGTAGCAATTAATGTCCTACTGGCACT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 GTACTTGATGATGGAGTGACACTTGTTTTAATACATCAGCCACATTATGTGTTAAATGC 657
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 AGACCTAACTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 CCATGCCAAATAAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCC
                                                                                                                                                                                                                                                                                                                                                                                                            298 ACATAATGCAGTACTTAATGTCCTACTGGCACTGCACTTGATGATGAGGAGTGACAGATGTT
                                                                                                       ;
0
                                                                      Length 170985;
                                                                 Score 89.8; DB 2; Length 17
Pred. No. 1.2e-07;
0; Mismatches 392; Indels
contig of 2453 bp in length
gap of unknown length
contig of 2298 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Homo sapiens clone Unpublished
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HTG; HTGS_PHASEL; HTGS_DRAFT.
HOMO sapiens.
93586: 0
93686: 0
95984:
                                                                 Query Match
Best Local Similarity 45.3%;
Matches 325; Conservative
91134
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AC022322/c
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8215 CIGITGCIATIGITGCITATIGITGCIGCIGITGCIGCIGCIGCIACIGITGCIG 8156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 TATITCITIATITATTAATGAATTAAGAGCTGTTCCATGTCCTGATGGTACTTAGACTCA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8395 CIGCIGCIACIGCIGCIGCIGCIGCIACIGCIGCIACIACIALGGIAATIATIGCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 CCAATGCAGGTGACTTAGCTACTTTAGCCACATAATGCAGTACTTAATGTCCTACTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8335 CTGCTGCTACTGTTGTTACTGTGATTTCTGTTGCTACTGCTGTTGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 TITITACIATAATGGTGGT-GCTGCTTAAGGAGAAGCTAATGGTAATTAACCTTTCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8455 IGTIGCTGATGCTGCTACTNGTTGCTAATGCTGTTGCTACTATTACTGTTGCTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 CAAATAATGCTGCTAGAGGTATATGTGTACCATGCCAAATAAACAGAGTAGGCTCTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 CTGCACITGATGATGAGTGACAGATGTTTTGATAGATCAGCCGCATAATGTGTTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 GCAAACCTAACTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 186935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 88.8; DB 2;
14.4%; Pred. No. 1.8e-07;
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90323. 135921
/note="assembly_name:Contig21"
136022. 186935
                                                                                                                                                                                                                                                                                                             'note="assembly_name:Contig15"
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31066. .40841
/note="assembly_name:Contigl7"
                                                                                                                                                                                                                                                                                                                                                                                                      40942. .52869
/note="assembly_name:Contig18"
52970. .63635
                                                                                                                                                                                                                     11893. .14813
/note="assembly_name:Contig13"
                                                                                                                                                                                                                                                         14914. .19837
/note="assembly_name:Contig14"
                                                                                                                                             5934. .8646
/note="assembly_name:Contigl1"
8747. .11792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="assembly_name:Contig19"
                                                                                                       1699. .5833
'note="assembly_name:Contig10"
                                                                                                                                                                                                  'note="assembly_name:Contig12"
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/note="assembly_name:Contig20
                                 1464, ,3253
/note="assembly_name:Contig8"
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/note="assembly_name:Contig22
                                                                                      'note="assembly_name:Contig9"
             /note="assembly_name:Contig7"
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40007 c 40377 g 51585 t
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Best Local Similarity 44.4%;
Matches 542; Conservative
                                                                      3354. .4598
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                                         Direct Submission
Submitted (30-JAN-2000) Genome Sequencing Center, Washington
Inversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 24, 2000 this sequence version replaced g1:7109575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown length
contig of 10666 bp in length
gap of unknown length
contig of 26487 bp in length
gap of unknown length
contig of 45599 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 186000; agarose-fp
Insert size: 185435; sum-of-contigs
Quality coverage: 6.94 in Q20 bases; agarose-fp
Quality coverage: 7.00 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length
contig of 2921 bp in length
gap of unknown length
contig of 4924 bp in length
gap of unknown length
contig of 4835 bp in length
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of 11928 bp in length
                                                                                                                                                                                                                                                            Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181940 bases at least 030
Consensus quality: 183253 bases at least 030
Consensus quality: 183254 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of unknown length
contig of 1790 bp in length
app of unknown length
contig of 1245 bp in length
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of 9776 bp in length
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gap of unknown length
contig of 3046 bp in length
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of 6093 bp in length
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contig of 1135 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 1363 bp in length
                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
                                                                                                                                                                                                                               Center project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .186935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-317M22"
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       2 (bases 1 to 186935)
Waterston, R.H.
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                                             TITLE
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                             AUTHORS
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A linear HTG 18-JUL-2002
*** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
8155 TIGTIGCTGCTCTTAITGTTGCTGCTGCTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTT 8096
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                                                                                                                                           929 CTAATTACTTTTTAATGGTAATTTCGAAGCAGGTAAAAGTTAATGTTTAAAGTGTCCAG
                                                                         8095 TTACTGCTGCTATTGTTGCTGTTGCTGATGCTGTTGCTGTTGCTGATACTGTTGC--
                                                                                                               AATGTAGCAATTAATGTCCTACTGGCACTGTACTTGATGATGGAGTGACACTTGTTTTA
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***, 70 unordered pieces.
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AC119627.2 GI:21746574
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Rattus norvegicus
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Durbin, K.J., Earnhart, C., Edgart, D., Edgards, C.C., Elhaj, C., Escetto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Fester, P., Frantz, P., Gortell, J.H., Guovara, W., Garratne, P., Hawes, A., Harnandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., Hannandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hannandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hannandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hollins, B., Jackson, B., Jia, Y., Juher, J., Huly, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Juher, J., Huly, S., Hume, J., Jackson, L.E., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisegd, H., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mawhiney, E., Martin, R., Martindale, A., Martin, M., Mabahwari, M., Mapua, P., Martin, R., Martindale, A., Martin, M., Moser, M., Neal, D., Martin, R., Martin, M., Mapua, P., Martin, R., Martin, R., Martin, R., Martin, M., Mayen, N., Nowlean, R., Nowlean, S., Ogh, M., Olyado, R., Pace, A., Payton, B., Savet, M., Pace, A., Payton, R., Savet, R., Pace, A., Paurerisa, K., Thomas, S., Stotton, A., Sotte, R., Paul, R., Pan, P., Tanesia, A., Malliams, G., Williams, G., Williams, G., Williams, G., Williams, G., Wall, Y., Wuly, Y., Wuly, 
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NOTE: This is a 'working draft' sequence. It currently
consists of 70 contigs. The true order of the places
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
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Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
Submitted (18-JUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, Tx 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20340348.

Center: Baylor College of Medicine
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Consensus quality: 134624 bases at least Q40
Consensus quality: 141279 bases at least Q30
Consensus quality: 145103 bases at least Q30
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Chemistry: Dye-terminator Big Dye: 100%
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-62L12
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Direct Submission
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Nuzny, D.M., Admans C., Adilo-Oduola, B., Adi-osman, F.R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Asc. J.R., Yapele, M., Banks, T., Barbaria, J., Benton, J., Bindsenburg, K., Bonnin, D., Bouck, J., Bowles, S. Bricker, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burchet, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Checko, J. Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Davilla, M.L., Bursis, C., Bary, Carroll, L., Dederlich, D., Anide, R., Delaney, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delagdo, O., Edwards, C.C., Elbaj, C., Escotto, M., Earlbarte, C., Edgart, D., Edwards, C.C., Elbaj, C., Escotto, M., Earlbarte, C., Edgart, D., Flagg, N., Ford, J., Poster, P., Frantz, P. Gorrell, J.H., Guevara, W., Gunarathe, P., Hans, A., Hamilton, K. Harris, C., Harris, K., Mayue, K., Martin, K., Wasquez, L., Patkers, R., Patkers, R., Patkers, R., Patkers, R., Patkers, R., Patkers, K., Barks, M., Rolas, M., Rolas, M., Rolas, M., Rolas, M., Solaeter, S., Scott, G., Taylor, T., Telfrod, B., Thomas, K., Warting, K., Wull, Y., Wull, Y., Wull, Y., Wull,
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Mammalia; Eutheria;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                          Worley, K.C.

Loases 1 to 191841)

Worley, K.C.

Direct Submission

Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 191841)

Worley, K.C.

Direct Submission
                                                                                                                                                                                                                Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced 91:20976298.
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Consensus quality: 127183 bases at least Q40
Consensus quality: 134210 bases at least Q30
Consensus quality: 134549 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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ACLIU817 204259 bp DNA linear HTG 29-JUL-2002 Mus musculus chromosome UNK clone RP23-155B20, WORKING DRAFT SAGDENCE, 16 unordered pieces.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 204259)
McPherson, J.D. and Waterston, R.H.
The Sequence of Mus musculus clone
Unpublished
2 (bases 1 to 204259)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 AIGCAGACCTAACTTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTA 713
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                                                                                                                                                                                                                                                                                                                                                                                                  294 ACCCACATAATGCAGTACTTAATGTCCTACTGGCACTGCACTTGATGATGGAGTGACAGA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 TGTTTTTGATAGATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTACTATAATGG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473
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                                                                                                                                                                                                                                                           174 TTAAGGAGAAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGCTGCTAGAGGTATATG 233
                                                                                                                   54 AAGAGCTGTTCCATGTCCTGATGGTACTTAGACTCAAGCTGGATTGACTGATGTAGGTGC 113
                                                                                                                                                                                       114 TECTGATCTTGGTACTTGTGTTAATTGCAGACCTAATTTTTACTATAATGGTGGTGCTGC 173
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 AGGIGITGCTGCCGTTACTAGTTAATGTGTACCTTGCCAACTAAACAAAAAAACGATTCTCC
                                               Score 88.4; DB 2; Length 191841;
pred. No. 2.2e-07;
0; Mismatches 386; Indels 0;
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104411: contig of 2903 bp in length
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AC110817.3 GI:21105087
HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FULLTOP.
                                                     6.7%;
                                                                                         Conservative
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AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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411 TGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTTTGCTGCTGGTGCTGCCGC 470
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3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig25"
70199 .100939
/note="assembly_name:Contig26"
10.1040 .131732_name:Contig27"
/note="assembly_name:Contig27"
/note="assembly_name:Contig28"
163982 .204259
/note="assembly_name:Contig28"
a 41663 c 41736 g 57836 t 15.
                                                                                                                                                                                                                                                                                                                                              20721. 30389 // Chote="assembly_name:Contig22" 30490. 38838 // Note="assembly_name:Contig23" 38939. 51519 // Note="assembly_name:Contig24" 51620. 70098
                                                                                                                                                                                                                                                                                 9742. .14703
/note="assembly_name:Contig20"
14804. .20620
/note="assembly_name:Contig21"
                                                                                                      /note="assembly_name:Contigl3"
1327. .2375
...ote="assembly_name:Contigl5"
                                                                                                                                                                                                         5977. ,7869
/note="assembly_name:Contig18"
7970. ,9641
                                                                                                                                                       2476. 3800
/note="assembly_name:Contig16"
                                                                                                                                                                                   3901. .5876 '--
/note="assembly_name:Contig17"
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/note="assembly_name:Contig19"
9742. .14703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87.6;
Pred. No. 36
                         organism="Mus musculus"
                                        /db_xref="taxon:10090'
                                                                         /clone="RP23-155B20'
                                                            /chromosome="UNK"
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             Direct Submission

Submitted (15-FEB-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

( Chases 1 to 20429) MCPherson, J. D. and Waterston, R. H.
                                                                                              Direct Submission
Submitted (29-JUL-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                          rkway, St. Louis, MO 63108, USA
May 23, 2002 this sequence version replaced gl:18874253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a "working draft" sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 10%
Sequencing vector: plasmid; 10%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-treminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198852 bases at least Q40
Consensus quality: 200032 bases at least Q20
Insert size: 211000; agarose-fp
Insert size: 203242; sum-of-contigs
Quality coverage: 8.38 in Q20 bases; sum-of-contigs
                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                        of 32049 bp in length
unknown length
of 40278 bp in length.
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of 9669 bp
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unknown 1
of 5817 b
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McPherson, J.D. and Waterston, R.H.
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Direct Submission

Direct Submission

Direct Submission

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
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Jiang,X., Song,L. and Roe,B.A.
Direct Submission
Submitted (21-FEB-2001) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                              1071 AGTACTTGATGATGGAACATCAACTAATTTTGTAGCTTCCGCAACTGAATGTACTAAATG 1130
                                                                                                                                                                                                                                                                                                                                                            ITCTGCTGGCTTTTTTGCATCAAAACAACTGGTTTTACAGCAGGTACTGATACATGTAC 1190
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Mus musculus BAC Clone rp23-11f20
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HTG; HTGS_PHASE1; HTGS_DRAFT
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/chromosome="6"
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/clone_lib="RPC1 - 23 Female (C57BL/6J) Mouse BAC Library"
63608 c 62531 g 67771 t 1222 others
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46.3%; Pred. No. 2.9e-07;
tive 0; Mismatches 374; Indels 3;
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E 1 (bases 1 to 84472)
S Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Legaspi, R., Maduro, C.E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, C.E., Masiello, C., Masirian, S. D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Sturgeon, C., Tomas, J.W., Thomas, P. J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L., H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                ACO96684 B4472 bp DNA linear HTG 22-SEP-2001
Takifugu rubripes clone 241N7, WORKING DRAFT SEQUENCE, 3 unordered
                                         598 GTACTTGATGATGGAGTGACACTTGTTTTTAATACATCAGCCACATTATGTGTTAAATGC 657
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Submitted (22-SEP-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                       658 AGACCTAACTTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov
Contact: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
Center project information
Center clone name: arc
Center clone name: 241N07

Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0,990319
Consensus quality: 83810 bases at least Q40
Consensus quality: 83810 bases at least Q40
Consensus quality: 83900 bases at least Q20
Insert size: 89000; agarcse-fp
Insert size: 89000; agarcse-fp
Insert size: 84272; sum-of-contigs
Quality coverage: 12.81x in Q20 bases; sun-of-contigs
Quality coverage: 13.53x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sum-of-contigs
                                                                                                                                                                                                           Db 102578 GCTGCTGTTGTTGTTGTTGCTGCTGCTGTTGTTGTTGCT 102619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                   718 TITGCTGCTGCTGCCGCTGCAGGTGTTGCTGCCGTTACT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                       AC096684.1 GI:15721942
HTG: HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 84472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takifugu rubripes.
Takifugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                seces
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                  RESULT 15
AC096684
LOCUS
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AUTHORS
TITLE
JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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4603 CIGCIGCIGCIACTACTGTIGCIGCTGTIGTIGTIGTIGTIGTIGTIGTIGTIGTIGTIGTIGGTG 4662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4663 CIGCIGCIACIGITGCIGITGCIGCIGCIGTIGITGCIGITGTIGITGCIGCIGCIG 4722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1723 CIGCIACIGITGITGCIGCIGCIGITGITGCIGCIGCIGTIGITGITGCIGCIGCIGTIGITG 4782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 AAGCIGGATIGACIGAIGTAGGIGCIGCIGAICTIGGIACTIGIGTAATIGCAGACCIA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1900 CIGCIGITGITGCIGCIGITGITGITGCIGCIGITGITGITGCIGCIGCIGITGCIG 4959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5080 TIGCIGITGITGITGITGCIGCIGCTACIGITGITGCIGCTGCIGITGTTGCIGCTGTTG 5139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ATTTTTACTATAATGGTGGTGCTGCTTAAGGAGAAGCTAATGGTAATTAACCTTTCGCAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 CAAATAATGCTGCTAGAGGTATATGTGTACCATGCCAAATAAACAGAGTAGGCTCTGTTA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 GCAAACCTAACTTTTACTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTTAAG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 ITTTTGCTGCTGCTGCTGCTGCAGGTGTTGCTGCCGTTACTAGTTAATGTGTACTT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 GCCAACTAAACAAAACGATTCTCCTGCCACTGCAGGTGCCTAAGCTAATTTAGCCACAT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 TTATTTCTTTATTATTAATGAATTAAGAGCTGTTCCATGTCCTGATGGTACTTAGACTC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAATGCAGGTGACTTAGCTACTTTAGCCACATAATGCAGTACTTAATGTCCTACTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4783 CTGTTGTTGCTGCTGCTGCTGTTTTTGTTGCTGCTACTGTTGTTGTTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCACTTGATGATGGAGTGACAGATGTTTTTGATAGATCAGCCGCATAATGTGTTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 AATGTAGCAATTAATGTCCTACTGGCACTGTACTTGATGATGAGGAGTGACACTTGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 ATACATCAGCCACATTATGTGTTAAATGCAGACCTAACTTTTACTATAATGGTGGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 84472;
1 10947: contig of 10947 bp in length 11047: gap of unknown length 8 37566: contig of 26519 bp in length 7 84472: contig of 46806 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 393; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 86.2; DB 2; 45.8%; Pred. No. 6.7e-07;
                                                                                                                                          1. .84472
/Organisam="Takifugu rubripes"
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                                                                                                                                                                                                                                 /clone_lib="Incyte Genomics"
1. 10947
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37667. .84472
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a 20937 c 21103 g 21384 t
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11048._37566
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                                                                                                                                                                                                                                                                                                                clone_end:T7
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tes 335; Conserv
                      10948
11048
37567
37667
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